

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 29, 2002, 09:42:16 : Search time 5865.16 Seconds
(without alignments)
17804.039 Million cell updates/sec

Title: US-09-676-436-3

Perfect score: 4990

Sequence: 1 ctgagagacttcctgatga.....ggttatttaggaagctc 4990

Scoring table: IDENTITY-NUC

Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 843946

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenBank:

- 1: gb_ba.*
- 2: gb_bt.*
- 3: gb_hg.*
- 4: gb_ov.*
- 5: gb_ov.*
- 6: gb_ov.*
- 7: gb_ov.*
- 8: gb_ov.*
- 9: gb_ov.*
- 10: gb_ov.*
- 11: gb_ov.*
- 12: gb_ov.*
- 13: gb_ov.*
- 14: gb_ov.*
- 15: gb_ov.*
- 16: gb_ov.*
- 17: gb_ov.*
- 18: gb_ov.*
- 19: gb_ov.*
- 20: gb_ov.*
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- 22: gb_ov.*
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- 25: gb_ov.*
- 26: gb_ov.*
- 27: gb_ov.*
- 28: gb_ov.*
- 29: gb_ov.*
- 30: gb_ov.*
- 31: gb_ov.*
- 32: gb_ov.*
- 33: gb_ov.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match Length	DB ID	Description
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1	29.6	0.6	87	3	DDTDND	M59747 D discoiden
2	25.2	0.5	100	6	AR007403	AR007403 Sequence
3	25.2	0.5	76	5	AF023584	AF023584 Paralich
4	25.2	0.5	70	1	AX033167	AX033167 Sequence
5	25.2	0.5	99	6	AF023584	AF023584 Sequence
6	25.2	0.5	99	6	AF023584	AF023584 Sequence
7	25.2	0.5	99	6	AF023584	AF023584 Sequence
8	24.8	0.5	92	4	RABPFRM18	RABPFRM18 Sequence
9	24.6	0.5	92	4	AX173377	AX173377 Sequence
10	24.6	0.5	71	6	AR140801	AR140801 Sequence
11	24.6	0.5	71	6	193480	193480 Sequence
12	24.6	0.5	71	6	193480	193480 Sequence
13	24.4	0.5	73	9	195107	195107 Sequence
14	24.4	0.5	73	9	S76509	S76509 DLS8 (A) lh
15	24.4	0.5	98	3	DNOTRANSTIN	DNOTRANSTIN Sequence
16	24.4	0.5	100	5	AR007408	AR007408 Sequence
17	24.4	0.5	51	10	U92173	U92173 Mus musculu
18	24.4	0.5	66	6	AX207310	AX207310 Sequence
19	24.4	0.5	88	9	AB048411	AB048411 Homo sapi
20	24.4	0.5	97	6	AR014521	AR014521 Sequence
21	24.4	0.5	97	6	PD010413	PD010413 Chimeric
22	23.8	0.5	82	4	AF294354S5	AF294354 Bos tauru
23	23.8	0.5	87	14	AF050514	AF050514 Human end
24	23.8	0.5	50	3	TRBAMPTC2	TRBAMPTC2 Sequence
25	23.8	0.5	51	10	MH0130784	MH0130784 Mus muscu
26	23.8	0.5	94	6	AX326634	AX326634 Sequence
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28	23.8	0.5	94	6	AX326634	AX326634 Sequence
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30	23.6	0.5	97	6	AS025850	AS025850 Homo sapi
31	23.6	0.5	97	6	AS025850	AS025850 Homo sapi
32	23.6	0.5	98	11	HUM0770A	HUM0770A Human STS
33	23.6	0.5	98	6	AX326603	AX326603 Sequence
34	23.6	0.5	98	6	AX059502	AX059502 Sequence
35	23.6	0.5	100	5	AF025983	AF025983 Paralich
36	23.4	0.5	77	6	A20465	A20465 oligonucleo
37	23.4	0.5	79	10	RATPLYC	RATPLYC Rat/polyoma
38	23.4	0.5	93	6	AX240522	AX240522 Sequence
39	23.4	0.5	88	9	S72771	S72771 immunoglobu
40	23.4	0.5	99	6	AX015186	AX015186 Sequence
41	23.2	0.5	99	11	HSPB49C03	AL033823 H. sapiens
42	23.2	0.5	87	5	CHKMILAS	M19461 Chicken C-m
43	23.2	0.5	97	4	OCJ72578	U72578 Cryptotlagus
44	23.2	0.5	100	5	AF174523	AF174523 Bufo dana
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97	23.2	0.5	91	9	HSJ32336	U32336 Human pre-B
98	23.2	0.5	91	9	HSJ32336	U32336 Human pre-B
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100	23.2	0.5	91	9	HSJ32336	U32336 Human pre-B

ALIGNMENTS

RESULT	1	DDTDND	D discoiden protein kinase 4 gene, partial cds.	87 bp	DNA	linear	INV 27-APR-1993
LOCUS	DDTDND	D discoiden protein kinase 4 gene, partial cds.	87 bp	DNA	linear	INV 27-APR-1993	
DEFINITION	DDTDND	D discoiden protein kinase 4 gene, partial cds.	87 bp	DNA	linear	INV 27-APR-1993	
ACCESSION	M59747	M59747.1	GI:167723				
VERSION	M59747.1	GI:167723					
KEYWORDS	protein kinase 4						
SOURCE	Dictyostellium discoideum (strain AX-3)	DNA					
ORGANISM	Dictyostellium discoideum						
REFERENCE	1	(bases 1 to 87)					
AUTHORS	Waribabu, B. and Duttin, R. P.						
TITLE	Identification of a protein kinase multigene family of Dictyostellium discoideum: Molecular cloning and expression of a cDNA encoding a developmentally regulated protein kinase						
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	88	1115-1119	(1991)			
MEDLINE	51142122						
FEATURES	Location/Qualifiers						
source	1..87						
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	/strain="AX-3"						
	/db_xref="taxon:44589"						
	<1..>87						

CDS

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/codon_start=1
/product="protein kinase 4"
/protein_id="AA33189.1"
/db_xref="GI:167724"
/translation="NLIDQYGHKLDGFGAKRITENKSMC"
BASE COUNT      36 a 12 c 14 g 25 t
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Query Match      0.6%  Score 29.6; DB 3; Length 87;
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Matches 50; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 4051 aaatctcttaccctcctggattcaaacctggagagatttcgatttcagtaag 4110
Db 1 NATCTTATATGATCATATGACATATTAACTCAGATGTTTGGATTGCAAAAAGA 60

QY 4111 ctcaaaacaatgccagaccatg 4134
Db 61 ATCAGAGAAATACCAAAAGTATG 84

RESULT 2
AR007403/c
LOCUS      AR007403      100 bp      DNA      linear      PAT 04-DEC-1998
DEFINITION      Sequence 4 from patent US 5750497.
ACCESSION      AR007403
VERSION      AR007403.1 GI:3966887
KEYWORDS      Unknown.
SOURCE      Unknown.
ORGANISM      Unclassified.
REFERENCE      1 (bases 1 to 100)
AUTHORS      Havelund,S., Halst.o slashed.m.J., Jonassen,I., Andersen,A.Sloth.
and Markussen,J.
TITLE      Acylated insulin
JOURNAL      Patent: US 5750497-A 4 12-MAY-1998;
FEATURES
source
1..100
/organism="unknown"
BASE COUNT      29 a 22 c 23 g 26 t
ORIGIN

Query Match      0.5%  Score 26; DB 6; Length 100;
Best Local Similarity 55.6%; Pred. NO. 1.7e+05;
Matches 50; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 4469 aagaatgaagctagtagaataatgacttggaataattcttcaactactgtatgtaa 4528
Db 97 AAGCTGACGACGTAAGGGTATCGTTGAACAATGTTGACTTCTATCTCTTCTTTGTAC 38

QY 4529 tattacataaagactgtcgaagaacg 4558
Db 37 CAATTGGAAAACACTACTGCTCTAGACGAC 8

RESULT 3
AF025984
LOCUS      AF025984      96 bp      DNA      linear      VRT 30-OCT-1997
DEFINITION      Paralicthys dentatus lactate dehydrogenase (LDHA) gene, allele
pLDHA2, intron 6.
ACCESSION      AF025984
VERSION      AF025984.1 GI:2570847
KEYWORDS      summer flounder.
SOURCE      Paralicthys dentatus
ORGANISM      Euryarchaea; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
Pleuronectoidae; Paralicthyidae; Paralicthys.
REFERENCE      1 (bases 1 to 96)
AUTHORS      Quattro,J.M. and Jones,W.J.

Amplification Primers That Target Locus-Specific Introns in
Actinopterygian Fishes
Unpublished
2 (bases 1 to 96)
Quattro,J.M. and Jones,W.J.
Direct Submission
Submitted (22-SEP-1997) Biological Sciences, University of South
Carolina, Coker Life Sciences Building, Columbia, SC 29208, USA
Location/Qualifiers
source
1..96
/organism="Paralicthys dentatus"
/db_xref="taxon:66718"
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/gene="LDHA"
/note="lactate dehydrogenase gene"
feature="pLDHA2"
1..96
/gene="LDHA"
/number=6
BASE COUNT      24 a 22 c 20 g 30 t
ORIGIN

Query Match      0.5%  Score 25.4; DB 5; Length 96;
Best Local Similarity 64.4%; Pred. NO. 2.4e+05;
Matches 38; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 4473 gccagccagctcctcgaccattcgtttgtcaagggtttgcacagatgaagaatgaagcct 4481
Db 14 GTGGACAAATCTTAGACGATTCATTTCACAAACAGTGTGCACATGATGATGTCCT 72

RESULT 4
AX033167
LOCUS      AX033167      70 bp      DNA      linear      BCT 21-SEP-2000
DEFINITION      Sequence 3 from Patent WO0045176.
ACCESSION      AX033167
VERSION      AX033167.1 GI:10280029
KEYWORDS
SOURCE      Escherichia coli.
ORGANISM      Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
REFERENCE      1 (bases 1 to 70)
AUTHORS      Gallusser,A., Karl,J., Lill,H., Stahl,P., Krueger,K. and Borgya,A.
TITLE      Method of identifying n-terminal probop
JOURNAL      Patent: WO 0045176-A 03-AUG-2000;
GALLUSSER ANDREAS (DE); KARL JOHANN (DE); LILL HELMUT (DE);
STAHL PETER (DE); KRUEGER KERSTIN (DE); BORGYA ANNELESE (DE);
ROCHE DIAGNOSTICS GMBH (DE)
Location/Qualifiers
source
1..70
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10 a 19 c 21 g 20 t
BASE COUNT      10 a 19 c 21 g 20 t
ORIGIN

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Best Local Similarity 62.9%; Pred. NO. 2.7e+05;
Matches 39; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1778 agggcgccgtcgtgatgaagcagatctaccaggttcacgtcgtcagaggaggttctctgaggagct 1837
Db 8 AGCGAGCTGTTCACCTGCTGCGACAGTTTACCTCTGCGAGGCTTACCTGCTTCC 67

QY 1838 tg 1839
Db 68 TG 69

RESULT 5
AX033159

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LOCUS	RABP1K418	83 bp	DNA linear	NAM 27-APR-1999
DEFINITION	Rabbit muscle phosphofructokinase gene, exon 18.			
ACCESSION	M14473.207202			
VERSION	M14473.1	GF:165622		
KEYWORDS	phosphofructokinase.			
SEGMENT	18 of 22			
ORGANISM	Rabbit (New Zealand) DNA, clone lambda-Charon 4APFX.			
ORGANISM	Oryctolagus cuniculus			
REFERENCE	Kuriyama, M. 1982. Chordata: Craniata: Vertebrata. Euteleostomi: Euteleostei. 10: 831. <i>Neogeny: Lepididae, Oryctolagus.</i>			
AUTHORS	Lee, C.-P., Kao, M.-C., French, B.A., Putney, S.D. and Chang, S.H.			
TITLE	The rabbit muscle phosphofructokinase gene: Implications for protein structure, function, cloning and tissue specificity			
JOURNAL	J. Biol. Chem.	262	4195-4199	(1987)
MEDLINE	87166033			
COMMENT	Draft entry and computer-readable sequence for [1] kindly provided by S.H. Chang. 02-Feb-1997.			
FEATURES	1..83	Location/Qualifiers		
SOURCE	1..83	Jorganism="Oryctolagus cuniculus" /db_xref="taxon:9986"		

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exon      16777       /number=18
intron    78..-83   /note=-PKF Intron P*
BASE COUNT      23 a 13 c 27 g 20 t
ORIGIN      About 719 bp after segment 17.

Query Match          0.5% ; Score 25; DB 4; Length 83;
Rest local similarity 61.5% ; Match NO. 3-le+05;
Matches 40; Conservative 0; Mismatches 25; Indels 0; Caps 0;

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[illegible]

TITLE	Skadopoulos M.H. and Iacobi: Use of recombinant parainfluenza viruses (pivs) as vectors to protect against infection and disease caused by p1v and other human pathogens			
JOURNAL	Patent: WO 0142445-A 31 14-JUN-2001: The Secretary of the Department of Health and Human Services (US)			
FEATURES	Location/Qualifiers 1. .92			
SOURCE	/organism="synthetic construct" /db_xref="taxon:32630" /note="Reverse primer for MSV A G gene insert"			
BASE COUNT	20 a	12 c	26 g	14 t
ORIGIN				
Query Match	0.5%	Score 24.8:	DB 6:	Length 92:


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DEFINITION Drosophila melanogaster DNA sequence, complete insertion sequence.
ACCESSION L20950
VERSION L20950.1 GI:304832
INFORMATION insertion sequence.
KEYWORDS Drosophila melanogaster
SOURCE Drosophila melanogaster
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 98)
AUTHORS Engels, W. K. and Johnson-Schlitz, D. M.
TITLE Deletion of the white allele: Transposase-induced derivative of
a white gene (1993)
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 98)
AUTHORS Johnson-Schlitz, D. M. and Engels, W. K.
TITLE P-element-induced interallelic gene conversion of insertions and
deletions in Drosophila melanogaster
JOURNAL Mol. Cell. Biol. 13, 7008-7018 (1993)
MEDLINE 94019372
FEATURES
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BASE COUNT 37 a 2 c 1 g 58 t
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Query Match 0.5% Score 24.4; DB 3; Length 98.
Best Local Similarity 56.1% Pred. NO. 4.5e+05;
Matches 46; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
Oy 1362 tctgactctctattttagaccctttgttagcaagcagtcgagatg999gttaaaaa 1421
Db 85 TATAAATATTATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 26
Oy 1422 attaatcttaagactcacaag 1443
Db 25 TTTAATTTAATAAATAATCATG 4
RESULT 14
AR007408/c
LOCUS AR007408 100 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 9 from patent US 5750497.
ACCESSION AR007408
VERSION AR007408.1 GI:3966892
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 100)
AUTHORS Rave, M. S., Halstr. O. slashed, M. J., Jonassen, I., Andersen, A. S. et al.
TITLE Activated Insulin
JOURNAL Patent: US 5750497-A 9 12-MAY-1998;
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        /organism="unknown"
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Best Local Similarity 54.4% Pred. NO. 4.5e+05;
Matches 49; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
Oy 4469 aagatgaagcctagtagaatatggatctggaaattctcttaataactactatgtatgaa 4528
Db 97 AAGCTGACGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 38
Oy 4529 tattacataaagaagctgctgtagaagcag 4558

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Db 37 CAATTGGAAACTACTGTGCTTAGACGCAG 8
RESULT 15
U92173/c
LOCUS U92173 51 bp mRNA linear ROD 19-FEB-1998
DEFINITION Mus musculus clone IC3 T cell receptor beta chain mRNA, partial
ACCESSION U92173
VERSION U92173.1 GI:2894946
KEYWORDS
SOURCE House mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 51)
AUTHORS Johnston, S. L. and Wettstein, P. J.
TITLE T cell receptor diversity in CTLs specific for the CTT-1 and CTT-2
minor histocompatibility antigens
JOURNAL J. Immunol. 159 (6), 2606-2615 (1997)
MEDLINE 97444147
REFERENCE 2 (bases 1 to 51)
AUTHORS Johnston, S. L. and Wettstein, P. J.
TITLE Direct Submission
JOURNAL Submitted (06-MAR-1997) Immunology, Mayo Clinic, 200 1st St S.W.,
Rochester, MN 55905, USA
FEATURES
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Matches 30; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Oy 1513 gaatttcagatctccatgtatgggttcagattatgtcagat 1552
Db 41 GTATTTCCAGATACCTCTCTCGGATCAGTCCAGGTGCACT 2
Search completed: May 25, 2002, 12:55:02
Job time: 11566 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 29, 2002, 10:21:32 : Search time 487.5 Seconds
(without alignments)
17574.160 Million cell updates/sec

Title: US-09-676-436-3
Perfect score: 4990
Sequence: 1 ctgaagactctccatga.....ggcttatattgaagagctc 4990
Scoring table: IDENTITY.MUC
Gapop.10.0, Gapext.1.0

Searched: 1736436 seqs, 858457221 residues
Total number of hits satisfying chosen parameters: 2046006

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2	/SIDSI/gcgdata/geneseq-emb1/NA1981.DAT :	2	/SIDSI/gcgdata/geneseq-emb1/NA1981.DAT :
3	/SIDSI/gcgdata/geneseq-emb1/NA1982.DAT :	3	/SIDSI/gcgdata/geneseq-emb1/NA1982.DAT :
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Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27.2	0.5	78	AAT50934	Mouse p53-recognt
2	26.6	0.5	92	AA19445	Human secreted pro
3	25.6	0.5	100	AA08600	Human insulin deri
4	25.2	0.5	70	AA18899	Human G-protein su
5	25.2	0.5	70	AA18899	Human brain natriu
6	25.2	0.5	89	AA18899	Human brain natriu
7	25.2	0.5	89	AA18899	Human brain natriu
8	25.2	0.5	99	AA18899	Human brain natriu
9	25.2	0.5	54	AA17346	Primer 307-3195 fo

C 10	25	0.5	91	22	ABA69691	Human foetal liver
C 11	24.8	0.5	77	21	AA13392	Human secreted pro
C 12	24.8	0.5	92	22	AA08600	Reverse PCR primer
C 13	24.8	0.5	94	21	AA11499	Human secreted pro
C 14	24.8	0.5	94	21	AA11541	Human secreted pro
C 15	24.6	0.5	71	18	AA165208	CDNA encoding grow
C 16	24.6	0.5	72	21	AA52344	CDNA encoding Dros
C 17	24.6	0.5	98	20	AA23469	Human neutrophil c
C 18	24.6	0.5	82	20	AA25128	801E Bundle peptid
C 19	24.4	0.5	99	22	ABA58615	Human foetal liver
C 20	24.4	0.5	100	25	AA35588	Probe 114054 for g
C 21	24.4	0.5	80	22	AA356411	Human insulin deri
C 22	24.4	0.5	80	22	AA356411	Human foetal liver
C 23	24.2	0.5	80	22	AA356411	Human brain expres
C 24	24.2	0.5	80	22	AA356411	Human brain expres
C 25	24.2	0.5	80	22	AA356411	Human brain expres
C 26	24.2	0.5	84	21	AA42397	Thymosin alpha-1 n
C 27	24.2	0.5	94	21	AA451645	Sbgl exon sequence
C 28	24.2	0.5	94	21	AA451668	Sbgl exon sequence
C 29	24.2	0.5	94	21	AA451692	Sbgl exon sequence
C 30	24.2	0.5	95	22	AA71915	Human foetal liver
C 31	24.2	0.5	95	22	AAK20302	Human brain expres
C 32	24.2	0.5	95	22	AA46381	Human bone marrow
C 33	24.2	0.5	95	22	AA152270	Probe 120956 used
C 34	24.2	0.5	99	22	ABA75243	Human foetal liver
C 35	24.2	0.5	99	22	ABA39902	Human foetal liver
C 36	24.2	0.5	99	22	AAK23782	Human brain expres
C 37	24.2	0.5	99	22	AAK49875	Human bone marrow
C 38	24.2	0.5	99	22	AA126980	Probe 116913 for g
C 39	24.2	0.5	99	22	AA157998	Probe 124484 used
C 40	24.2	0.5	66	22	AA014229	Synthetic transcri
C 41	24.2	0.5	66	22	AA014229	Cell death protect
C 42	24.2	0.5	66	22	AA014229	Gene 124484 used in
C 43	24.2	0.5	97	16	AA081937	SSP5 11.11.11.1
C 44	24.2	0.5	97	16	AA081937	Synthetic storage
C 45	24.2	0.5	97	20	AAV95532	Synthetic lysine-r

ALIGNMENTS

RESULT 1	
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ID	AA150934 standard: cDNA: 78 BP.
AC	AA150934:
DT	07-APR-1997 (first entry)
DE	Mouse p53-recognition clone 1 5' sequence.
XX	p53 binding protein: Mdmx, tumour suppressor; cancer; ss
XX	Mus sp.
PN	MO9641875-A1.
XX	
PD	27-DEC-1996.
XX	
PF	13-JUN-1996: 96MO-NL00239.
XX	
PR	13-JUN-1995: 95EP-0201565.
XX	
PA	(INTR-) INTROGENE BV.
XX	(UYLE-) RIJKSUNIV LEIDEN
PI	Jochimsen A. Snavits A. Van Der Eb AJ.
XX	
DR	WPI: 1997-063462/06.
XX	
PT	Nucleic acid encoding p53-binding protein - which has homology to
XX	Mouse Mdm2, for use in cancer research


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RESULT 15
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ID AAT65208 standard; DNA: 71 BP.
XX
XX AC AAT65208:
XX
XX DT 10-SEP-1997 (first entry)
XX
XX DE Transforming growth factor beta-1 binding ligand D 11.
XX
XX KW Transforming growth factor: beta-1; TGF-beta-1; binding ligand;
KW identification; SELEX; anti-mitogenic; inhibition; cell;
KW Systematic Evolution of Ligands by Exponential enrichment;
KW epithelial; proliferation; diagnosis; treatment; fibroids;
KW kidney; lung; liver; dermal scarring; restenosis; ss.
XX
XX OS Synthetic.
XX
XX PN W09618579-Al.
XX
XX PD 05-DEC-1996.
XX
XX PF 30-MAY-1996; 96WO-US08014.
XX
XX PR 20-MAR-1996; 96US-0618693.
XX
XX PR 02-JUN-1995; 95US-0458423.
XX
XX PR 02-JUN-1995; 95US-0458424.
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XX PR 05-JUN-1995; 95US-0465591.
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XX PR 05-JUN-1995; 95US-0465594.
XX
XX PR 07-JUN-1995; 95US-0479725.
XX
XX PR 07-JUN-1995; 95US-0479783.
XX
XX PA (NEXS-) NEXSTAR PHARM INC.
XX
XX PI Gold L, Janjic N, Pogratis N, Ringquist S, Toothman PJ;
XX WPI; 1997-034387/03.
XX
XX PT Identification of nucleic acid ligands to TGF-beta, PDGF and bNGF
XX using SELEX. used in the diagnosis and treatment of proliferative
XX disorders
XX
XX PS Claim 15; Page 123; 209pp; English.
XX
XX CC The present sequence, a transforming growth factor beta-1
XX (TGF-beta-1) binding ligand, was identified by Systematic Evolution
XX of Ligands by Exponential enrichment (SELEX). Briefly a candidate
XX mixture of nucleic acids was contacted with TGF-beta-1, and nucleic
XX acids having an increased affinity to TGF-beta-1 partitioned from
XX the remainder of the mixture. The partitioned nucleic acids were
XX then amplified to yield a mixture of nucleic acids enriched for
XX sequences with higher affinity and specificity for binding to
XX TGF-beta-1. The ligand is anti-mitogenic and may be used to inhibit
XX epithelial cell proliferation, or in the diagnosis and treatment of
XX TGF-beta-1 mediated pathological conditions, e.g. fibrotic
XX conditions such as fibroids of the kidney, lung and liver and more
XX acute conditions such as dermal scarring and restenosis.
XX
XX SQ Sequence 71 BP; 15 A; 16 G; 22 C; 18 T; 0 other;

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Query Match 0.5%; Score 24.6; DB 18; Length 71;
Best Local Similarity 65.5%; Pred. No. 5.7e+03;
Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
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DB 56 GAAGACGTAACTAGTAGTATTAAACATACCCCCCTCGCCCGCATCGCTCTCC 2

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Search completed: May 29, 2002, 13:05:25
Job time: 9833 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 29, 2002, 09:11:38 : Search time 3518.59 Seconds
(without alignments)
19141.135 Million cell updates/sec

Title: US-09-676-436-3

Perfect score: 4990

Sequence: 1 ctgaagacttcctgatga.....ggttattttagaagctc 4990

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 297742

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: em_esthm.*
3: em_esthm.*
4: em_esthm.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_hic.*
9: gb_est1.*
10: gb_est2.*
11: gb_hic.*
12: gb_gsa.*
13: em_gss_hum.*
14: em_gss_inv.*
15: em_gss_pln.*
16: em_gss_vrt.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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5	27.8	0.6	83	A1360096	B1063432
6	27.8	0.6	94	B1322285	k19a08.y
7	27.8	0.6	100	AA154655	aa154655
8	27.4	0.5	91	T85845	aa154655
9	27.4	0.5	98	A1054386	aa154655
10	26.8	0.5	100	CS3310	aa154655
11	26.6	0.5	81	BE573242	aa154655
12	26.6	0.5	82	BF101686	aa154655
13	26.4	0.5	87	AA267457	aa154655
14	26.4	0.5	95	AA946634	aa154655
15	26.4	0.5	95	R93104	aa154655
16	26.2	0.5	78	R40354	aa154655
17	26.2	0.5	93	AV551027	aa154655

18	26.2	0.5	93	IC	T62011
19	26	0.5	98	1C	B1850011
20	26	0.5	98	17	BH127076
21	26	0.5	98	9	AA85746
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45	25.8	0.5	98	9	AA85746

ALIGNMENTS

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LOCUS aa58f02.r1 Soares_thymus_2NDMT Mus musculus cDNA clone
DEFINITION IMAGE:1361691.5 mRNA sequence
ACCESSION AA990067
VERSION AA990067.1 GI:317543
KEYWORDS EST
SOURCE house mouse
ORGANISM Mus musculus

REFERENCE
AUTHORS
Marrin, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Norris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R., and Waterston, R.
Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus.
1 (bases 1 to 95)
GenBank accession number: U00000.1

TITLE
JOURNAL
COMMENT
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
Washington University School of Medicine
7444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: mmarra@wustl.edu
This clone is available royalty-free through IMAGE Consortium (info@imgc.llnl.gov) for further information.
WCI:699731
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 82
Location/Qualifiers
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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_image="1361691"
/clone_lib="Soares_thymus_2NDMT"
/sex="male"

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/strain="C57BL/6J"
/db_xref="taxon:10090"
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/sex="male"

Email: M-SaberePRCU.EUN.EG
Seq primer: SK.

Location/Qualifiers
1. .95

/organism="Schistosoma mansoni"

/strain="Egyptian"

/db.xref="taxon:6183"

/clone="SMTBADAH50038SK"

/clone.lib="S. mansoni cDNA"

/lab.host="E. coli XL Blue1"

/note="vector: pBluescript II SK+; Site 1: EcoRI; Site 2:

XhoI; mRNA was purified from adult couples of S. mansoni.

cDNA was constructed and cloned simultaneously using

vector priming with the pBluescript II SK+ vector. cDNA

was directionally synthesized from the EcoRI site in the

vector to the XhoI site.

31 a 15 c 10 g 39 t

BASE COUNT
ORIGIN

Query Match 0.5%; Score 26.4; DB 10; Length 95;
Best Local Similarity 59.2%; Pred. No. 7.3e+04;
Matches 45; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

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Db 5 ACTATGATTATTATACACTAGTTCAGCAATCCCTTATCTATAAAATGTTATCTTTATT 64

Qy 701 tcaagtcgactatg 716

Db 65 TCAATTTTACCATAG 80

Search completed: May 29, 2002, 11:17:02
Job time: 7404 sec

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C 3	25.2	0.5	99	US-08-427-091-5	Sequence 5, Appl
C 4	25.2	0.5	99	US-08-427-091-5	Sequence 5, Appl
C 5	24.6	0.5	71	US-08-878-957-8	Sequence 7, Appl
C 6	24.6	0.5	71	US-08-438-423A-78	Sequence 7, Appl
C 7	24.6	0.5	71	US-08-973-124-78	Sequence 7, Appl
C 8	24.6	0.5	71	US-08-973-124-78	Sequence 7, Appl
C 9	24.6	0.5	72	PCT-US96-08014-78	Sequence 7, Appl
C 10	24.6	0.5	72	US-09-100-664A-5	Sequence 8, Appl
C 11	24.4	0.5	100	US-08-400-256-9	Sequence 9, Appl
C 12	24	0.5	100	US-08-975-365-9	Sequence 9, Appl
C 13	24	0.5	97	US-08-182-175A-53	Sequence 54, Appl
C 14	24	0.5	97	US-08-474-633A-64	Sequence 54, Appl
C 15	23.8	0.5	97	PCT-US92-06412-54	Sequence 54, Appl
C 16	23.6	0.5	83	US-08-672-158A-8	Sequence 8, Appl
C 17	23.6	0.5	87	US-08-631-751A-4	Sequence 8, Appl
C 18	23	0.5	77	US-07-679-052A-8	Sequence 6, Appl
C 19	23	0.5	60	US-08-643-704A-17	Sequence 17, Appl
C 20	22.8	0.5	94	US-09-344-888A-8	Sequence 8, Appl
C 21	22.8	0.5	96	US-08-246-583-9	Sequence 9, Appl
C 22	22.6	0.5	95	US-08-484-322-5	Sequence 5, Appl
C 23	22.6	0.5	77	US-07-679-052A-10	Sequence 10, Appl
C 24	22.4	0.4	90	US-08-133-702-1	Sequence 21, Appl
C 25	22.4	0.4	95	US-08-332-766A-41	Sequence 41, Appl
C 26	22.4	0.4	97	US-08-182-175A-48	Sequence 48, Appl
C 27	22.4	0.4	57	US-08-474-633A-57	Sequence 57, Appl
C 28	22.4	0.4	97	PCT-US92-06412-48	Sequence 48, Appl

Qy 4469 aagaaatqaaacctaagtag

4469 အနုပညာပို့ဆောင်ရေးဦးစီးဌာန၊ အထွေထွေအဖွဲ့အစည်း

Qy 4469 aaqaa:qaauccclaglagahlalggactlqgaahltctcttaatcactactgtatgtaa 4528

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Db 97 AAGTCGACGCTAGGATGATCGTGAACAACTGTTGACTTCTATCTGTTCTTGTAC 38
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RESULT 2
US-08-975-365-4/C
; Sequence 4, Application US/08975365
; Patent No. 6011007
; GENERAL INFORMATION:
; APPLICANT: Havelund, Svend
; APPLICANT: Halstrom, John
; APPLICANT: Jonassen, Ib
; APPLICANT: Andersen, Asger sloth
; APPLICANT: Markussen, Jan
; TITLE OF INVENTION: ACYLATED INSULIN
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6011007o, No. 6011007disk of No. 6011007th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,365
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/400,256
; FILING DATE: 03-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 3985.220-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-975-365-4

Query Match 0.58; Score 26; DB 3; Length 100;
Best Local Similarity 55.6%; Pred. No. 6.1e+02;
Matches 50; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

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Db 37 CAATTGGAAACTACTGCTGCTTAGACCGAG 8

RESULT 3
US-08-427-097-5
; Sequence 5, Application US/08427097
; Patent No. 5668294
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; GENERAL INFORMATION:
; APPLICANT: Meagher, Richard B.
; APPLICANT: Summers, Anne O.
; TITLE OF INVENTION: Metal Resistance Sequences and
; TITLE OF INVENTION: Transgenic Plants
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/427,097
; FILING DATE: 21-APR-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 40-94
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Oligonucleotide"
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-427-097-5

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Best Local Similarity 54.3%; Pred. No. 1e+03;
Matches 51; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

Qy 3026 atgctcgtactaaatgtgagagtgtgtagaggtacagaccacagtggtggcgaactcaaggat 3085
Db 2 AAGACCCAGCTATAGGTGAGCTGTACTCTGCTTTCGATGGAAGGCATTGAAATGCC 61
Qy 3086 ttgattttctacaagcaattgaaactgcctttat 3119
Db 62 GTGACCATACTCAAGCAAGCCCAAGTTGCCCTATAT 95

RESULT 4
US-08-878-957-5
; Sequence 5, Application US/08878957
; Patent No. 5965796
; GENERAL INFORMATION:
; APPLICANT: Meagher, Richard B.
; APPLICANT: Summers, Anne O.
; APPLICANT: Rugh, Clayton L.
; TITLE OF INVENTION: Metal Resistance Sequences and
; TITLE OF INVENTION: Transgenic Plants
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: US
; ZIP: 80303
```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC compatible
SOFTWARE: DOS/MS-DOS
CURRENT APPLICATION DATA: Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/878.957
FILING DATE: 19-JUNE-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/427,097
FILING DATE: 21-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Perbet, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 40-94A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-878-957-5

Query Match 0.58; Score 25.2; DB 2; Length 99;
Best Local Similarity 54.3%; Pred. No. 1e-03; Mismatches 43; Indels 0; Gaps 0;
Matches 31; Conservative 0;
QY 3026 atctctgactgaatgagagtgtagggatgacagaccaggtggagcgcacaggaat 3085
DB 2 AAGACCCAGCTATAGGTGAAGCTGTTACTGCTGCTATTCGATCGAAGGCGATGAGTCC 61
QY 3086 tggatcttctacagcaatgagacctgttat 3119
DB 62 GTGAGCATACTCAAGCAAGCAAGTTCGCTATAT 95

RESULT 5
US-08-458-423A-78/C
Sequence 78, Application US/08458423A
Patent No. 5731424
GENERAL INFORMATION:
APPLICANT: PENELOPE J. TOOTHMAN
APPLICANT: STEVEN RINGQUIST
TITLE OF INVENTION: HIGH AFFINITY TGFA NUCLEIC
TITLE OF INVENTION: ACID LIGANDS AND INHIBITORS
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
FILING DATE: 2-JUNE-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/458.423A
FILING DATE: 2-JUNE-1995
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,991
FILING DATE: 8-SEPTEMBER-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931,473
FILING DATE: 17-AUGUST-1992
ATTORNEY/AGENT INFORMATION:
NAME: Diane H. McClellan
REGISTRATION NUMBER: 33,960
REFERENCE/DOCKET NUMBER: NEX 34-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3433
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 71 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-458-423A-78

Query Match 0.58; Score 24.6; DB 1; Length 71;
Best Local Similarity 65.5%; Pred. No. 1.2e-03;
Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 3558 gacactgattagctctatctcaagcggatgacattgcgacatccctcc 4012
DB 56 GAAGACGTAGTAGTAGTAGTATTAAACATACCCCTCCGCGCATGCTCTCC 2

RESULT 6
US-08-458-424B-78/C
Sequence 78, Application US/08458424B
Patent No. 5731424
GENERAL INFORMATION:
APPLICANT: PENELOPE J. TOOTHMAN
APPLICANT: STEVEN RINGQUIST
TITLE OF INVENTION: HIGH AFFINITY TGFA NUCLEIC
TITLE OF INVENTION: ACID LIGANDS AND INHIBITORS
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
FILING DATE: 2-JUNE-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
CLASSIFICATION: 536

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1 FILING DATE: 05-JUNE-1995
2 PRIOR APPLICATION DATA:
3 APPLICATION NUMBER: 08/465,591
4 FILING DATE: 05-JUNE-1995
5 PRIOR APPLICATION DATA:
6 APPLICATION NUMBER: 08/479,725
7 FILING DATE: 07-JUNE-1995
8 PRIOR APPLICATION DATA:
9 APPLICATION NUMBER: 08/479,783
10 FILING DATE: 07-JUNE-1995
11 PRIOR APPLICATION DATA:
12 APPLICATION NUMBER: 08/618,693
13 FILING DATE: 20-MARCH-1996
14 ATTORNEY/AGENT INFORMATION:
15 NAME: Barry J. Swanson
16 REGISTRATION NUMBER: 33,215
17 REFERENCE/DOCKET NUMBER:
18 TELECOMMUNICATION INFORMATION:
19 TELEPHONE: (303) 793-3333
20 TELEFAX: (303) 793-3433
21 INFORMATION FOR SEQ ID NO: 78:
22 SEQUENCE CHARACTERISTICS:
23 LENGTH: 71 base pairs
24 TYPE: nucleic acid
25 STRANDEDNESS: single
26 TOPOLOGY: linear
27 MOLECULE TYPE: DNA
28 US-08-973-124-78
29
30 Query Match 0.5% Score 24.6; DB 4; Length 71:
31 Best Local Similarity 65.5% Pred. NO. 1.2e+03;
32 Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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Query Match: 0.5%, Score 28.0, 06; Length 71.
Best Local Similarity 65.5%, Pred. NO. 1.26+03;
Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 3958 gaacatgtgattgagctgtattcaaaacagatcacattgcatcaagctctcc 4012
||||| ||| ||||| ||| ||| ||| ||||| |||
DB 56 GAAGACGTAGTAGTAGTATTAAAAACATACCCCCCTGGCCGATGCTCTCC 2

RESULT 8
PCT-US96-08014-78/c
; Sequence 78, Application PC/TUS9608014
; GENERAL INFORMATION:
; APPLICANT: LARRY GOLD; NEDUSA JANJIC; STEVEN RINGQUIST; NIKOS
; APPLICANT: PAGRATIS; PENELOPE J. TOOTHMAN
; TITLE OF INVENTION: HIGH AFFINITY OLIGONUCLEOTIDE
; TITLE OF INVENTION: LIGANDS TO TRANSFORMING GROWTH
; TITLE OF INVENTION: FACTOR (TGF ), PLATELET-DERIVED
; TITLE OF INVENTION: GROWTH FACTOR (PDGF) AND HUMAN
; TITLE OF INVENTION: KERATINOCYTE GROWTH FACTOR (hKGF)
; NUMBER OF SEQUENCES: 304
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/08014
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/458,423
; FILING DATE: 02-JUNE-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/458,424
; FILING DATE: 02-JUNE-1995

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TELECOMMUNICATION INFORMATION:
TELEPHONE 401.487.5800
TELEFAX 203.443.1684
TELEX 133521
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 72 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
US-09-100-664A-5

Query Match 0 5%: Score 24.6; DB 3; Length 72;
Best Local Similarity 59.2% Pred. N1.3e-03;
Matches 42; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

3694 atcgagagagccagatggaggggtgctacacgtcatcagctgcagaccggggagctg 3753
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1 ATAGATCGGAGTCGTGCGCCACATCTACTCTGGGCACCCAGCATCAACACTGCCGAGCAG 60

3754 atggcccgatgaa 3764
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61 CTGCCCATCAA 71

```

RESULT 10
 US-08-400-256-9/c
 : Sequence 9. Application US/08400256
 : Patent NO. 5750497
 : GENERAL INFORMATION:
 : APPLICANT: Havelund, Svend
 : APPLICANT: Halstrom, John
 : APPLICANT: Jonassen, Ib
 : APPLICANT: Andersen, Asser Sloth
 : APPLICANT: Andersen, Arne
 : TITLE OF INVENTION: ACYLATED INSULIN
 : NUMBER OF SEQUENCES: 49
 : CORRESPONDENCE ADDRESS:

COMMERCIAL: NO. 5750497 disk of NO. 5750497th America, Inc.
 ADDRESS: NO. 5750497 No. 5750497 disk of NO. 5750497th America, Inc.
 STREET: 405 Lexington Avenue, 64th Floor
 CITY: New York
 STATE: New York
 COUNTRY: United States of America
 ZIP: 10174-6401
 COMPUTER READABLE FORM:
 SERIAL TYPE: IBM PC Compatible
 COMPUTER OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/400,256
 FILING DATE: 03-MAR-1995
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Lambdis, Elias J.
 REGISTRATION NUMBER: 33,728
 REFERENCE/DOCKET NUMBER: 3985,220-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-867-0123
 TELEFAX: 212-878-9655
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 100 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 US-08-400-256-g

RESULT 13
US-08-474-633A-63
Sequence 63: Application US/08474633A
Patent No. 577691
GENERAL INFORMATION:
APPLICANT: COMPANY: DU PONT DE NEMOURS AND
APPLICANT: COMPANY: CHIMERIC GENES AND
TITLE OF INVENTION: METHODS FOR INCREASING
TITLE OF INVENTION: INCREASING THE LYSINE
TITLE OF INVENTION: AND THREONINE CONTENT
TITLE OF INVENTION: OF THE SEEDS OF PLANTS
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS
ADDRESS: AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474.633A
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: BARBARA C. SIEGELL
REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB-1037-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4931
TELEFAX: 302-773-0164
TELEX: 835420
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: E. coli
CELL TYPE: DHS alpha
IMMEDIATE SOURCE:
CLONE: 92.2
FEATURES:
FEATURE KEY: CDS
LOCATION: 2..88
OTHER INFORMATION: /function= "synthetic
OTHER INFORMATION: storage protein
OTHER INFORMATION: /product= "protein"
OTHER INFORMATION: /gene= "ssp"
OTHER INFORMATION: /standard_name= "5.11.11.5"
US-08-474-633A-63

Query Match 0.5% Score 24: DB 1: Length 97:
Best Local Similarity 58.3% Pred. No. 2.2e+03:
Matches 42: Conservative 0: Mismatches 30: Indels 0: Gaps 0:
Qy 1120 ggtatgaggtggtgacacagaggaattaaaggaattggaagtagtagtagtagtag 1179
DB 10 GACATGAGGCGCATGCGAGGAGGATCAAGTGGCA-GGAGGAGAGATCAAGTGGATGGA 69
Qy 1180 agtgaagagaa 1191
DB 70 AGAGAGATGAA 81

RESULT 14
PCT-US92-06412-54
Sequence Information: Application PC/TUS9206412
General Information:
APPLICANT: Saverio Carl Falco
APPLICANT: Sharon J. Keeler
APPLICANT: Janet A. Rice
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containin
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: USA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06412
FILING DATE: 19920807
CLASSIFICATION: 530
PRIORITY INFORMATION:
PRIORITY NUMBER: 07/743,006
FILING DATE: 9 August 1991
ATTORNEY/AGENT INFORMATION:
NAME: Linda Asmethyl Floyd
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: BB-1031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 992-4929
TELEFAX: (302) 892-7949
TELEX: 835420
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: E. coli
CELL TYPE: DHS alpha
IMMEDIATE SOURCE:
CLONE: 92.2
FEATURES:
FEATURE KEY: CDS
LOCATION: 2..88
OTHER INFORMATION: /function= "synthetic storage protein
OTHER INFORMATION: /product= "protein"
OTHER INFORMATION: /gene= "ssp"
OTHER INFORMATION: /standard_name= "5.11.11.5"
PCT-US92-06412-54

Query Match 0.5% Score 24: DB 5: Length 97:
Best Local Similarity 58.3% Pred. No. 2.2e+03:
Matches 42: Conservative 0: Mismatches 30: Indels 0: Gaps 0:
Qy 1120 ggtatgaggtggtgacacagaggaattaaaggaattggaagtagtagtagtag 1179
DB 10 GACATGAGGCGCATGCGAGGAGGATCAAGTGGCA-GGAGGAGAGATCAAGTGGATGGA 69
Qy 1180 agtgaagagaa 1191
DB 70 AGAGAGATGAA 81

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 29, 2002, 09:42:16 ; Search time 5865.16 seconds
(without alignments)
17804.019 Million cell updates/sec

Title: US-09-676-436-3

Perfect score: 4990

Sequence: 1 cttagagactctccagatga.....gctttatttaggaagctc 4990

Scoring table:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 1046326293 residues

Total number of hits satisfying chosen parameters: 843946

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenBank:

1: gb.ba.*

2: gb.htg.*

3: gb.in.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pl.*

9: gb.pr.*

10: gb.rc.*

11: gb.rgs.*

12: gb.sv.*

13: gb.un.*

14: gb.vi.*

15: ea.ba.*

16: ea.fun.*

17: ea.hum.*

18: ea.in.*

19: ea.ju.*

20: ea.mv.*

21: ea.or.*

22: ea.ov.*

23: ea.pat.*

24: ea.ph.*

25: ea.pl.*

26: ea.ro.*

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36: ea.htg.*

37: ea.htg.*

38: ea.htg.*

39: ea.htg.*

40: ea.htg.*

41: ea.htg.*

42: ea.htg.*

43: ea.htg.*

44: ea.htg.*

45: ea.htg.*

pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
1	87	87	AX-3*	/organism="Dictyostellium discoideum"
2	87	87	AX-3*	/db_xref="taxon:44689"
3	87	87	AX-3*	Location/Qualifiers

1	29.6	0.6	87	3	D01DDKD	M59747 D. discoideu
2	26.6	0.5	100	6	AX027403	AX027403 Sequen
3	25.4	0.5	96	5	AX025984	AX025984 Paralic
4	25.2	0.5	70	1	AX033167	AX033167 Sequence
5	25.2	0.5	70	6	AX033159	AX033159 Sequence
6	25.2	0.5	99	6	165769	165769 Sequence 5
7	25.2	0.5	83	4	RABPKM18	M14473 Rabbit musc
8	24.8	0.5	92	6	AX173377	AX173377 Sequence
9	24.6	0.5	71	6	AR140801	AR140801 Sequence
10	24.6	0.5	71	6	193480	193480 Sequence 78
11	24.6	0.5	71	6	193480	193480 Sequence 78
12	24.4	0.5	73	9	S76509	S76509 DisB (A) (h
13	24.4	0.5	98	3	U007408	L20950 Drosophila
14	24.4	0.5	100	5	AR007408	AR007408 Sequence
15	24.4	0.5	51	10	U92173	U92173 Mus musculu
16	24.4	0.5	66	6	AX207310	AX207310 Sequence
17	24.4	0.5	88	9	AB048405	AB048405 Homo sapi
18	24.4	0.5	97	6	AB014621	AB014621 Sequence
19	24.4	0.5	97	6	B0010413	B0010413 Chimeric
20	24.4	0.5	97	6	126754	126754 Sequence 54
21	23.8	0.5	82	4	AF294354	AF294354 Bos tauru
22	23.8	0.5	87	14	AF050514	AF050514 Human end
23	23.8	0.5	87	14	AF050514	AF050514 Human end
24	23.8	0.5	87	14	AF050514	AF050514 Human end
25	23.8	0.5	87	14	AF050514	AF050514 Human end
26	23.8	0.5	87	14	AF050514	AF050514 Human end
27	23.8	0.5	87	14	AF050514	AF050514 Human end
28	23.8	0.5	87	14	AF050514	AF050514 Human end
29	23.6	0.5	87	14	AF050514	AF050514 Human end
30	23.6	0.5	87	14	AF050514	AF050514 Human end
31	23.6	0.5	87	14	AF050514	AF050514 Human end
32	23.6	0.5	87	14	AF050514	AF050514 Human end
33	23.6	0.5	87	14	AF050514	AF050514 Human end
34	23.6	0.5	87	14	AF050514	AF050514 Human end
35	23.4	0.5	87	14	AF050514	AF050514 Human end
36	23.4	0.5	87	14	AF050514	AF050514 Human end
37	23.4	0.5	87	14	AF050514	AF050514 Human end
38	23.4	0.5	87	14	AF050514	AF050514 Human end
39	23.4	0.5	87	14	AF050514	AF050514 Human end
40	23.4	0.5	87	14	AF050514	AF050514 Human end
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42	23.4	0.5	87	14	AF050514	AF050514 Human end
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44	23.4	0.5	87	14	AF050514	AF050514 Human end
45	23.4	0.5	87	14	AF050514	AF050514 Human end

ALIGNMENTS

RESULT	1	87 bp	DNA	linear	INV 27-APR-1993
LOCUS	D01DDKD	D. discoideum protein kinase 4 gene, partial cda.			
DEFINITION	D. discoideum protein kinase 4 gene, partial cda.				
ACCESSION	M59747				
VERSION	M59747.1	GI:167724			
KEYWORDS	protein kinase 4				
SOURCE	Dictyostellium discoideum				
ORGANISM	Dictyostellium discoideum				
REFERENCE	Zukaryota: Mycetozoa: Dictyostellida: Dictyostellium				
ABSTRACT	(bases 1 to 87)				
TITLE	Identification of protein kinase multigene family of Dictyostellium discoideum: Molecular cloning and expression of a cDNA encoding a developmentally regulated protein kinase				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 88, 1115-1119 (1991)				
MEDLINE	91142122				
FEATURES	Location/Qualifiers				
source	1.. 87				
CDs	/organism="Dictyostellium discoideum"				
	/strain="AX-3"				
	/db_xref="taxon:44689"				
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/codon_start=1
/product="protein kinase 4"
/protein_id="AAA33189.1"
/db_xref="GI:167724"
/tranlation="NULLDYGHIKLTDFGFAKRIITENKSMC"
BASE COUNT      36 a  12 c  14 g  25 t
ORIGIN

Query Match      0.6%; Score 29.6; DB 3; Length 87;
Best Local Similarity 59.5%; Pred. No. 1.8e+04;
Matches 50; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Qy 4051 aaatcttccttaccctctgtgattatcaactgggagattttggtgattcagtaag 4110
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Db 1 AATCTAATTAATGATCATATGATGACATATTAAAGCTCACAGATTGTGGATTGCGAAGA 60

Qy 4111 ctcaaaacaatgccagaccatg 4134
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 61 ATCAGACAGATACCAAAAGATG 84

RESULT 2
AR007403/c
LOCUS      AR007403      100 bp      DNA      linear      PAT 04-DEC-1998
DEFINITION Sequence 4 from patent US 5750497.
ACCESSION AR007403
VERSION   AR007403.1 GI:3966887
KEYWORDS  Unknown.
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 100)
AUTHORS   Havelund S., Halstr. o slashed m.J., Jonassen I., Andersen, A. Sloth.
          and Markussen T.
TITLE     Acylated insulin.
JOURNAL   Patent: US 5750497-A 4 12-MAY-1998;
          Location/Qualifiers
FEATURES   source
            29 a  22 c  23 g  26 t
            /organism="unknown"

Query Match      0.5%; Score 26; DB 6; Length 100;
Best Local Similarity 55.6%; Pred. No. 1.7e+05;
Matches 50; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

Qy 4469 aagaatgaactagtgaatagatggactggaaattctcttaaccactactgtatgtaa 4528
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 97 AAGCTGAGACGCTAGGATGCTGTTGACATGTTGACTTCTATCTGTTCTTTGTAC 38

Qy 4529 tattacataagactgtgtgagagcag 4558
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 37 CAATTGAAAAGTACTGTGCTTAGACGCAG 8

RESULT 3
AF025984
LOCUS      AF025984      96 bp      DNA      linear      VMT 30-OCT-1997
DEFINITION Paralicthys dentatus lactate dehydrogenase (LDHA) gene, allele
          PdLDHA2, Intron 6.
ACCESSION AF025984
VERSION   AF025984.1 GI:2570847
KEYWORDS  summer flounder.
SOURCE    Paralicthys dentatus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
          Acanthomorpha; Acanthopterygii; Percormorpha; Pleuronectiformes;
          pleuronectoidae; Paralicthidae; Paralicthys.
REFERENCE 1 (bases 1 to 96)
AUTHORS   Quattro, J.M. and Jones, W.J.

Amplification Primers That Target Locus-Specific Introns in
Actinopterygian Fishes
Unpublished
REFERENCE 2 (bases 1 to 96)
AUTHORS   Quattro, J.M. and Jones, W.J.
TITLE     Direct Submission
JOURNAL   Submitted (22-SEP-1997) Biological Sciences, University of South
          Carolina, Coker Life Sciences Building, Columbia, SC 29208, USA
FEATURES   Location/Qualifiers
            source
              1..96
              /organism="Paralicthys dentatus"
              /db_xref="taxon:66718"
            gene
              1..96
              /gene="LDHA"
              /note="lactate dehydrogenase gene"
              /allele="PdLDHA2"
            intron
              1..96
              /gene="LDHA"
              /number=6
BASE COUNT      24 a  22 c  20 g  30 t
ORIGIN

Query Match      0.5%; Score 25.4; DB 5; Length 96;
Best Local Similarity 64.4%; Pred. No. 2.4e+05;
Matches 38; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 4423 gccagccagcclccgaccattgtttgtcgaagtttgcacagatgaagatgaagcct 4481
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 14 GICGGACAATCTAGACGATTCTTACAAAACAGCTGTCCACATGATGATGACGTCTCT 72

RESULT 4
AX033167
LOCUS      AX033167      70 bp      DNA      linear      BCT 21-SEP-2000
DEFINITION Sequence 3 from Patent WO0045176.
ACCESSION AX033167
VERSION   AX033167.1 GI:10280029
KEYWORDS  Escherichia coli.
SOURCE    Escherichia coli.
          Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
          Escherichia.
REFERENCE 1 (bases 1 to 70)
AUTHORS   Gallusser, A., Karl, J., Lill, H., Stahl, P., Krueger, K. and Borgya, A.
TITLE     Method of identifying n-terminal probnp
JOURNAL   Patent: WO 0045176-A 03-AUG-2000;
          GALLUSSER, ANDREAS (DE) ; KARL, JOHANN (DE) ; LILL, HELMUT (DE) ;
          STAHL, PETER (DE) ; KRUEGER, KERSTIN (DE) ; BORGYA, ANNELEISE (DE) ;
          ROCHE DIAGNOSTICS GMBH (DE)
          Location/Qualifiers
FEATURES   source
            1..70
            /organism="Escherichia coli"
            /db_xref="taxon:562"
BASE COUNT      10 a  19 c  21 g  20 t
ORIGIN

Query Match      0.5%; Score 25.2; DB 1; Length 70;
Best Local Similarity 62.9%; Pred. No. 2.7e+05;
Matches 39; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Qy 1778 agggcgccctgctatgaagcagctaccagttcatgtgcagagagttcttgagagact 1837
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 8 AGCCAGCTCTGTTCAACCTGCAGCTTCCGACAGATTACCTCGACAGTGGTACCGCTGTTC 67

Qy 1838 tg 1839
||
Db 68 TG 69

RESULT 5
AX033159

```

LOCUS AX033159 70 bp DNA linear PAT 21-SEP-2000
 DEFINITION Sequence 3 from Patent WO0045176.
 ACCESSION AX033159
 VERSION AX033159.1 GI:10280023
 KEYWORDS
 SOURCE Escherichia coli.
 ORGANISM Bacteria; Proteobacteria; gamma subdivision, Enterobacteriaceae; Escherichia.
 REFERENCE 1 (bases 1 to 70)
 AUTHORS Galluszer A., Keri J., Lill H., Stahl P., Krueger R. and Borgya A.
 TITLE Method of identifying a terminal probop
 JOURNAL PATENT 4,817,273 05-AGO-1990
 PATENT 4,817,273 05-AGO-1990
 STANDARDS STANL PETER (DE); KRUEGER KENSTIN (DE); BORGYA ANNELEISE (DE);
 MEDLINE ROCHE DIAGNOSTICS GREN (DE)
 FEATURES
 source 1 70
 Location/Qualifiers
 /organism="Escherichia coli"
 /db_xref="taxon:562"
 BASE COUNT 10 a 19 c 21 g 20 t
 ORIGIN

Query Match 0.5% Score 25.2; DB 6; Length 70;
 Best Local Similarity 62.9%; Pred. No. 2.7e+05;
 Matches 39; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
 Oy 1778 agggcgctgctgagcagctactaccagctcagctcagctgagctgagctgagct 1837
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 8 AGGGAGGCTGCTGAGCAGCTACTACCGCTCAGCTGAGCTGAGCTGAGCTGAGCT 67
 Oy 1838 tg 1839
 ||
 Db 68 TG 69

RESULT 6
 LOCUS 165769 99 bp DNA linear PAT 07-OCT-1997
 DEFINITION Sequence 5 from patent US 5668294.
 ACCESSION 165769
 VERSION 165769.1 GI:2482239
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 99)
 AUTHORS Koehler R.B. and Summers A.O.
 TITLE Metal resistance sequences and transgenic plants
 JOURNAL Patent: US 5668294-A 5-16-SEP-1997;
 FEATURES
 source 1 99
 Location/Qualifiers
 /organism="unknown"
 BASE COUNT 29 a 21 c 25 g 24 t
 ORIGIN

Query Match 0.5% Score 25.2; DB 6; Length 99;
 Best Local Similarity 58.3%; Pred. No. 2.8e+05;
 Matches 51; Conservative 0; Mismatches 43; Indels 0; Gaps 0;
 Oy 3026 atgcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 3085
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 2 AAGGCCAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 61
 Oy 3085 ttgattttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 3119
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 62 GTGAGCTACTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 95

RESULT 7
 RABPFM18

LOCUS RABPFM18 81 bp DNA linear MM 27-APR-1993
 DEFINITION Rabbit muscle phosphofructokinase gene, exon 18.
 ACCESSION M14473 J02702
 VERSION M14473.1 GI:165622
 KEYWORDS Phosphofructokinase.
 SEGMENT 18 of 22
 SOURCE Rabbit (New Zealand) DNA, clone lambda-Charon 4APFK.
 ORGANISM Oryctolagus cuniculus
 REFERENCE 1 (bases 1 to 83)
 AUTHORS Fracet B.A., Putney S.D. and Chang S.H.
 TITLE Rabbit muscle phosphofructokinase gene. Implications for
 JOURNAL Protein structure, function and tissue specificity
 MEDLINE J Biol Chem. 262: 4195-4199 (1987)
 COMPIPT 87166033
 by S.H.Chang, 02-FEB-1987.

FEATURES
 source 1 83
 Location/Qualifiers
 /organism="Oryctolagus cuniculus"
 /db_xref="taxon:9986"
 <1..15
 /note="PFK intron Q"
 16..77
 /number=18
 78..>83
 /note="PFK intron R"
 23 a 13 c 27 g 20 t
 BASE COUNT About 719 bp after segment 17.
 ORIGIN

Query Match 0.5% Score 25; DB 4; Length 83;
 Best Local Similarity 61.5%; Pred. No. 3.1e+05;
 Matches 40; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
 Oy 1737 gaggcttaccagctgctgagggctgtaaggagctgctgagggcgctgctgctgaa 1796
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 18 GAATGTCACACCTGCTGCAAGATGACAGAGCAGCTGTGAGAGAGAGCGCTTGGCTGAG 77
 Oy 1797 gcaat 1801
 |||||
 Db 78 GACT 82

RESULT 8
 AX173377/c
 LOCUS AX173377 92 bp DNA linear PAT 03-JUL-2001
 DEFINITION Sequence 31 from Patent WO0142445.
 ACCESSION AX173377
 VERSION AX173377.1 GI:14598152
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM artificial sequence.
 REFERENCE 1 (bases 1 to 92)
 AUTHORS Murphy R.R., Collins P.L., Schmidt A.C., Durbin A.P.,
 Skladopoulos M.H. and Tan T.
 TITLE Use of recombinant parainfluenza viruses (pivs) as vectors to
 protect against infection and disease caused by piv and other human
 pathogens
 JOURNAL Patent: WO 0142445-A 31 14-JUN-2001;
 The Secretary of the Department of Health and Human Services (US)
 FEATURES
 source 1 92
 Location/Qualifiers
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="Reverse primer for MSV A G gene insert"
 BASE COUNT 20 a 12 c 26 g 34 t
 ORIGIN

Query Match 0.5% Score 24.8; DB 6; Length 92;

RESULT	11
195107/c	
LOCUS	71 bp DNA
DEFINITION	Sequence 78 from patent US 5731434.
ACCESSION	195107 linear PAT 01-DEC-1998

RESULT 13
DROTRANSIN/C

98 bp DNA linear INV 05-JAN-1994

LOCUS DROTRANSIN

XX Example 3: Column 17-18; 71pp: English.

XX The invention relates to a nucleic acid molecule comprising a coding

XX sequence for an organometal resistance protein, which is operably

XX linked downstream of and under the regulatory control of a

XX plant-expressible transcription and translation regulatory sequence.

XX The organometal resistance gene is especially the merA gene from the

XX transposon Tn1 or the E. coli merB gene. merA encodes a mercuric ion

XX reductase and merB encodes a organomercurial lyase. The nucleic acid

XX sequences are useful for producing transgenic plants which are capable

XX of efficiently processing mercury. These plants are able to remove or

XX detoxify metal compounds such as methyl mercury and ionic mercury from

XX soil, sediment, and aquatic environments providing an efficient

XX bioremediation of metals and metalloids contaminated sites.

XX This sequence is especially useful for generating transgenic plants

XX gene which is mutated by random mutagenesis (see AA228584-128589 for

XX mutated sequences) and the mutated sequences are expressed in the

XX transgenic plants of the invention.

XX

XX Sequence 99 BP; 29 A; 21 C; 25 G; 24 T; 0 other:

XX

Query Match: 0.54; Score 25.2; DB 20; Length 99;

Best Local Similarity: 54.34; Pred. No. 4.7e+01;

Matches: 51; Conservative: 0; Mismatches: 43; Indels: 0; Gaps: 0;

OY 3036 atgtctgactaatatgtagagtgtagaggtacaaagaccaggtgagcagctcaggat 3085

DB 2 agaccagctataggtagagtgtagaggtacaaagaccaggtgagcagctcaggat 3119

OY 3086 ttgattttacaaagcaattgaaccgctcttat 3119

DB 62 gtgacatactcaagcaagcaagtgctctatat 95

RESULT 9

ID AA73946/C

XX AA73946 standard; DNA: 54 BP.

XX

XX AA73946;

XX

XX 06-DEC-2000 (first entry)

XX

XX GFP Leu(CTG)5 forward primer.

XX

XX Green fluorescent protein; GFP; reporter gene; codon utilisation;

XX Translational efficiency; protein abundance; PCR primer: 56.

XX

XX Synthetic.

XX

XX WO200042215-A1.

XX

XX 20-JUL-2000.

XX

XX 07-JAN-2000; 2000WO-AU00008.

XX

XX 08-JAN-1999; 99AU-0008078.

XX

XX (UTOU) UNIV QUEENSLAND.

XX

XX (SUNX) SUN X.

XX

XX Zhou J. Fraser 18;

XX

XX WPI: 2000-499118/44.

XX

XX Determining translational efficiency of codons in cells, comprising

XX introducing synthetic constructs with reporter genes fused in frame to

XX tandem repeats of the codon, and measuring expression -

XX

XX Example 1; Page 103, 190pp; English.

XX

XX The present sequence is a primer used to generate a synthetic gfp gene by

CC PCR amplification of a humanised gfp gene. A single artificial start

CC codon followed by a stretch of five identical codons was fused in frame

CC immediately upstream of a gfp coding sequence to form the synthetic gene.

CC The amplified fragment was cloned into the mammalian expression vector

CC pCMV3, which contains SV40 ori and the CMV promoter, and was used in a

CC method for determining the translational efficiency of a codon in a cell.

CC The synthetic construct was introduced into COS-1 cells and expression of

CC the reporter protein (green fluorescent protein) was measured. A series

CC of 54 gfp reporter constructs was made in which the gfp gene is preceded

CC in frame by a tandem repeat of 5 identical codons. The series covers the

CC entire set of 64 acceptable codon triplets. Codons with a higher

CC translational efficiency than their corresponding synonymous codons can

CC be identified; these codons may then be used to replace the test

CC preferred codon of a polynucleotide in a reporter gene. The test

CC expression with an undifferentiated epithelial cells such as COS-1 cells.

XX

XX Sequence 54 BP; 9 A; 14 C; 20 G; 11 T; 0 other:

XX

Query Match: 0.54; Score 25; DB 21; Length 54;

Best Local Similarity: 59.49; Pred. No. 3.6e+03;

Matches: 34; Conservative: 0; Mismatches: 15; Indels: 0; Gaps: 0;

OY 2732 ccagtccagcgcgtccatccaaagctttgcagcagcgtgaagcagtgatgc 2780

DB 53 ccattgacagctgctccctcccttgcctcagcagcagcagcagcagctggtac 5

RESULT 10

ID ABA6969/C

XX ABA6969 standard; DNA: 91 BP.

XX

XX ABA6969;

XX

XX 01-FEB-2002 (first entry)

XX

XX Human foetal liver single exon nucleic acid probe #17996.

XX

XX Human: foetal liver; gene expression; single exon nucleic acid probe: 55.

XX

XX HOMO sapiens.

XX

XX WO200157277-A2.

XX

XX 09-AUG-2001.

XX

XX 30-JAN-2001; 2001WO-US20665.

XX

XX 04-FEB-2000; 2000US-0180312.

XX

XX 26-MAY-2000; 2000US-3207456.

XX

XX 30-JUN-2000; 2000US-0608408.

XX

XX 03-AUG-2000; 2000US-0632385.

XX

XX 21-SEP-2000; 2000US-0234687.

XX

XX 27-SEP-2000; 2000US-0236339.

XX

XX 04-OCT-2000; 2000US-0024253.

XX

XX (MODE-) MOLECULAR DYNAMICS INC.

XX

XX Penn SG, Hanzel DK, Chen W, Rank DR.

XX

XX WPI: 2001-483447/52

XX

XX Human genome-derived single exon nucleic acid probes useful for

XX analyzing gene expression in human fetal liver.

XX

XX Claim 4, SEQ ID NO 17996; 633pp + sequence listing; English.

XX

XX The invention relates to a single exon nucleic acid probe for

XX measuring human gene expression in a sample derived from human foetal

XX liver. The single exon nucleic acid probes may be used for predicting,

XX measuring and displaying gene expression in samples derived from human

XX (fetal) liver. The present sequence is a single exon nucleic acid

XX probe of the invention.

RESULT 15
AAT65208/C
ID AAT65208 standard; DNA: 71 BP.
XX AC AAT65208;
XX DT 10-SEP-1997 (first entry)
XX DE Transforming growth factor beta-1 binding ligand D 11.
XX KW Transforming growth factor; beta-1; TGF-beta-1; binding ligand;
XX KW identification; SELEX; anti-mitogenic; inhibition; cell;
XX KW Systematic Evolution of Ligands by EXponential enrichment;
XX KW epithelial; proliferation; diagnosis; treatment; fibroids;
XX KW kidney; lung; liver; dermal scarring; restenosis; as.
XX OS Synthetic.
XX PN WO9618579-A1.
XX PD 05-DEC-1996.
XX PF 30-MAY-1996; 96WO-US08014.
XX PR 20-MAR-1996; 96US-0618693.
XX PR 02-JUN-1995; 95US-0458423.
XX PR 02-JUN-1995; 95US-0458424.
XX PR 05-JUN-1995; 95US-0465591.
XX PR 05-JUN-1995; 95US-0465594.
XX PR 07-JUN-1995; 95US-0479725.
XX PR 07-JUN-1995; 95US-0479783.
XX PA (NEXS-) NEXSTAR PHARM INC.
XX PI Gold L. Janjic N. Pagnatis M. Ringquist S. Toothman RJ;
XX DR WPI: 1997-034387/03.
XX PT Identification of nucleic acid ligands to TGF-beta, PDGF and hKGF
XX PT using SELEX, used in the diagnosis and treatment of proliferative
XX PT disorders
XX PS Claim 15: Page 123: 209pp: English.
XX CC The present sequence, a transforming growth factor beta-1
XX CC (TGF-beta-1) binding ligand, was identified by Systematic Evolution
XX CC of Ligands by Exponential enrichment (SELEX). Briefly a candidate
XX CC mixture of nucleic acids was contacted with TGF-beta-1, and nucleic
XX CC acids having an increased affinity to TGF-beta-1 partitioned from
XX CC the remainder of the mixture. The partitioned nucleic acids were
XX CC then amplified to yield a mixture of nucleic acids enriched for
XX CC sequences with higher affinity and specificity for binding to
XX CC TGF-beta-1. The ligand is anti-mitogenic and may be used to inhibit
XX CC epithelial cell proliferation, or in the diagnosis and treatment of
XX CC TGF-beta-1 mediated pathological conditions, e.g. fibrotic
XX CC conditions such as fibroids of the kidney, lung and liver and more
XX CC acute conditions such as dermal scarring and restenosis.
XX SQ Sequence 71 BP: 15 A: 16 C: 22 G: 18 T: 0 other;

Query Match 0.58; Score 24.6; DB 18; Length 71;
Best Local Similarity 65.5%; Pred. No. 5.7e-03;
Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 3958 gacacgtatgagcgtatccaaagcagcaccatcgacatcgacgtcc 4012
DB 56 GAGACGTAGTACTAGTATTTAAACATATACCCGCCGCGCGTGCCTCC 2

Search completed: May 29, 2002, 13:05:25
Job time: 9833 sec

SITE-2: ECO RI: Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NBHM; pregnant uterus NBHPU, and fetal heart NBHFI94) were mixed, and ss circles were made *in vitro*. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."

19	340488	345479,	and 484488-489479."
	16 c	15 g	20 t

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Query Match      0.68: Score 29; DB 9; Length 70;
Best Local Similarity 71.7%; P: 0.14e+04;
Matches 38; Conservative 15; Mismatches 15; Indels 0; Gaps 0;

CQ 4051 aaatctctcttaccctcctcgtggaataacaaactcygagattttggatgttc 4103
Db      |||||
8 ATATCTTCCTCCTCACTCAAGTGAAGTGAATTTGGGACACTTTGGATCTGC 60

```

SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1. (bases 1 to 71)
TITLE	NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap . National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL	Unpublished (1997)
COMMENT	Contact: Robert Strauszberg, Ph.D. Email: cgapb-re@mail.nih.gov Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D.

```

FEATURES
source
High quality sequence stop: 70.
Location/Qualifiers
1..71
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="IMAGE:2400828"
/clone_lib="NCI_CGAP_Kid12"
/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH10n"
/note="organ: kidney; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not 1; Site_2: Eco RI;
P.said DNA from the normalized library NCI_CGAP_Kid5 was
prepared, and as circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 1323912-1325831, 1471368-1472903 and
1492104-1493255). Subtraction by Bento Soares and M.
Fatma Bonaldo."
22 a 16 c 7 g 26 t

```


Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and

M., Huilsmann, M., Kucab, I., Le, N., Lemmon, G., Muller, P., Peterson, R., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevas, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.

DB 66 TAAA 7C
111

RESULT 12

NOT FOR
TITLE

[illegible]

Query Match

AR267951
LOCUS

ACCESSION
NUMBER

ORGANISM MUS Eukary

DB 66 TAAA 7C
111

ORGANISM

22105

Query Match

RESULT 13

Email: M.Sabere@RCU.EUN.DG

Seq primer: sk

Location/Qualifiers

FEATURES

Source
1..95
/organism="Schistosoma mansoni"
/strain="egyptian"
/db_xref="taxon:6183"
/clone="SMTBADM50038SK"
/clone_lib="S. mansoni cDNA"
/lab_host="E. coli XL Blue"
/note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
XhoI; mRNA was purified from adult couples of S. mansoni.
cDNA was constructed and cloned simultaneously using
vector priming with the pBluescript II SK+ vector. cDNA
was directionally synthesized from the EcoRI site in the
vector to the XhoI site."
BASE COUNT 31 a 15 c 10 g 39 t
ORIGIN

Query Match 0.58; Score 26.4; DB 10; Length 95;
Best Local Similarity 59.28; Pred. No. 7.3e+04;
Matches 45; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
QY 641 acctcttttatacagccctcagccatccagctattattattataaataacattt 700
DB 111
5 ACTATGATTATTATACACTACTTCAGCAATCCCTATCTATATAAATGTATCTTATTT 64
QY 701 tcaaatcgactatgg 716
111
DB 65 TGAATTTTACCATAG 80

Search completed: May 29, 2002, 11:17:02
Job time: 7404 sec

Fri Jun 6 11:22:53 2003

us-09-676-436-3.s21m100.rni

Page 1

GenCore version 4.5
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ON nucleic - nucleic search, using a model

Run On: May 29, 2002, 10:15:51 ; Search time 94.14 Seconds
(without alignments)

Title: US-09-676-436-3

Perfect score: 4990
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STORING LABEL: IDENTIFI_NDK
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Total number of hits satisfying chosen parameters: 613725

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 03

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA : *

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
C 1	26	0.5	100	1	US-08-400-256-4	Sequence 4, Appl
C 2	26	0.5	100	3	US-08-975-365-4	Sequence 4, Appl
C 3	25.2	0.5	99	1	US-08-447-097-5	Sequence 5, Appl
C 4	25.2	0.5	99	2	US-08-878-957-5	Sequence 5, Appl
C 5	24.6	0.5	71	1	US-08-458-423A-78	Sequence 78, Appl
C 6	24.6	0.5	71	1	US-08-459-424B-78	Sequence 78, Appl
C 7	24.6	0.5	71	4	US-08-973-124-78	Sequence 78, Appl
C 8	24.6	0.5	71	5	PCR-US96-08014-78	Sequence 78, Appl
C 9	24.6	0.5	72	3	US-09-100-664A-5	Sequence 5, Appl
C 10	24.4	0.5	100	1	US-08-400-256-9	Sequence 9, Appl
C 11	24.4	0.5	100	3	US-08-975-365-9	Sequence 9, Appl
C 12	24	0.5	97	1	US-08-152-175A-54	Sequence 54, Appl
C 13	24	0.5	97	1	US-08-446-633A-63	Sequence 63, Appl
C 14	24	0.5	97	5	PCR-US92-06412-54	Sequence 54, Appl
C 15	23.8	0.5	81	2	US-08-831-175A-8	Sequence 8, Appl
C 16	23.6	0.5	81	2	US-08-831-175A-8	Sequence 8, Appl
C 17	23.4	0.5	77	1	US-09-879-052A-8	Sequence 8, Appl
C 18	23	0.5	60	4	US-08-643-704A-17	Sequence 17, Appl
C 19	23	0.5	94	4	US-09-344-088A-0	Sequence 8, Appl
C 20	22.8	0.5	96	3	US-08-246-581-9	Sequence 9, Appl
C 21	22.8	0.5	96	3	US-08-464-322-5	Sequence 9, Appl
C 22	22.6	0.5	77	1	US-07-679-052A-10	Sequence 10, Appl
C 23	22.4	0.4	90	1	US-08-123-702-21	Sequence 21, Appl
C 24	22.4	0.4	94	2	US-08-332-766A-41	Sequence 41, Appl
C 25	22.4	0.4	97	1	US-08-182-175A-48	Sequence 48, Appl
C 26	22.4	0.4	97	1	US-08-474-633A-57	Sequence 57, Appl
C 27	22.4	0.4	97	1	PCR-US92-06412-48	Sequence 48, Appl

Query Match: 0.58; Score 25; CB 1: Length 100;
Best Local Similarity 55.6%; Pred. No. 6.ie+02;

DY 4169 aaqaatqaaagccctagaftagaattatatggaacttgccttcacctaaccatacaca +528

ACKNOWLEDGMENTS

RESULT 1
 US-08-400-256-4/C
 Sequence 4: Application US/08/00256
 Patent No. 5750497
 GENERAL INFORMATION:
 APPLICANT: Havelund, Svend
 APPLICANT: Halnstrum, John
 APPLICANT: Jonassen, Ib
 APPLICANT: Aardsen, Jan Sloth
 APPLICANT: Markussen, Jan
 TITLE OF INVENTION: ACYLATED INSULIN
 NUMBER OF SPOUNCES: 49
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: No. 5750497a No. 5750497diak of No. 5750497th America, Inc.
 STREET: 405 Lexington Avenue, 64th Floor
 CITY: New York
 STATE: New York
 COUNTRY: United States of America

ZIP: 10174-6401
COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release 11.0, Version 11.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/100.256
FILING DATE: 03-MAR-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Lambilis, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 3985,220-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-978-9655
INFORMATION FOR SEQ TO NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 100 base pairs
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
400-256.4

US-08-400-256-4

Db 97 AAGTCTGACACCTAAGGGTATCGTGAACAATGTTGTAATCTCTCTCTTTGTAAC 38

Qy 4529 tattacataaagactgctgctgagaagcag 4528

Db 37 CAATTGGAAAACACTACTGCTGTAGACGCAG 8

RESULT 2

US-08-975-365-4/C

; Sequence 4, Application US/08975365

; Patent No. 6011007

; GENERAL INFORMATION:

; APPLICANT: Havelund, Svend

; APPLICANT: Halstrom, John

; APPLICANT: Jonassen, Ib

; APPLICANT: Andersen, Aaser Sloth

; APPLICANT: Markussen, Jan

; TITLE OF INVENTION: ACYLATED INSULIN

; NUMBER OF SEQUENCES: 49

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: No. 60110070 No. 6011007disk of No. 6011007th America, Inc.

; STREET: 405 Lexington Avenue, 64th Floor

; CITY: New York

; STATE: New York

; COUNTRY: United States of America

; ZIP: 10174-6401

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/975,365

; FILING DATE:

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/400,256

; FILING DATE: 03-MAR-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Lambiris, Elias J.

; REGISTRATION NUMBER: 33,728

; REFERENCE/DOCKET NUMBER: 1985.220-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-867-0123

; TELEFAX: 212-878-9655

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 100 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA

US-08-975-365-4

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Best Local Similarity 55.6%; Pred. No. 6.1e+02;

Matches 50; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

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Db 97 AAGTCTGACACCTAAGGGTATCGTGAACAATGTTGTAATCTCTCTTTGTAAC 38

Qy 4529 tattacataaagactgctgctgagaagcag 4528

Db 37 CAATTGGAAAACACTACTGCTGTAGACGCAG 8

RESULT 3

US-08-427-097-5

; Sequence 5, Application US/08427097

; Patent No. 5668294

; GENERAL INFORMATION:

; APPLICANT: Meagher, Richard B.

; APPLICANT: Sommers, Anne O.

; TITLE OF INVENTION: Metal Resistance Sequences and

; TITLE OF INVENTION: Transgenic Plants

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.

; STREET: 5370 Manhattan Circle, Suite 201

; CITY: Boulder

; STATE: CO

; COUNTRY: US

; ZIP: 80303

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/427,097

; FILING DATE: 21-APR-1995

; CLASSIFICATION: 80Q

; ATTORNEY/AGENT INFORMATION:

; NAME: Feiber, Donna M.

; REGISTRATION NUMBER: 33,878

; REFERENCE/DOCKET NUMBER: 4C-94

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (303) 499-8080

; TELEFAX: (303) 499-8089

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 99 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: Other nucleic acid

; DESCRIPTION: /desc = "Oligonucleotide"

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

US-08-427-097-5

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Best Local Similarity 54.3%; Pred. No. 1e+03;

Matches 51; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

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Qy 3086 ttgattttctcaagcaattgaacctgccttat 3119

Db 62 GTGAGCATACTCAGCAAGCCAGTTCCTATAT 95

RESULT 4

US-08-878-957-5

; Sequence 5, Application US/08878957

; Patent No. 5965796

; GENERAL INFORMATION:

; APPLICANT: Meagher, Richard B.

; APPLICANT: Summers, Anne O.

; APPLICANT: Rugh, Clayton L.

; TITLE OF INVENTION: Metal Resistance Sequences and

; TITLE OF INVENTION: Transgenic Plants

; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.

; STREET: 5370 Manhattan Circle, Suite 201

; CITY: Boulder

; STATE: Colorado

; COUNTRY: US

; ZIP: 80303

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release 11.0, Version 11.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/878,957
 FILING DATE: 19-JUN-1997
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/427,097
 FILING DATE: 21-APR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Ferber, Donna M.
 REGISTRATION NUMBER: 33,878
 REFERENCE/DOCKET NUMBER: 40-34A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 499-8080
 TELEFAX: (303) 499-8089
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 99 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
 DESCRIPTION: /desc = "oligonucleotide"
 HYPOTHEICAL: NO
 ANTI-SENSE: NO
 US-08-878-957-5

Query Match 0.54: Score 25.2; DB 2; Length 99;
 Best Local Similarity 54.34; Pred. No. 10-03;
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Qy 3026 atgctcctgaactgaatgagtgagtgaggtacagaccaggggggagctcaaggat 3085
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Qy 3086 ttgattttctcaagcgaactgaacctgctttat 3119
 Db 62 GTGAGCATCTACGAGCAAGCCAGTTCCTATAT 95

RESULT 5
 US-08-458-423A-78/C
 Sequence 78: Application US/08/458423A
 Patent No. 5731424
 GENERAL INFORMATION:
 APPLICANT: PENELOPE J. TOOTHMAN
 APPLICANT: STEVEN RINGQUIST
 TITLE OF INVENTION: HIGH AFFINITY IGFA NUCLEIC
 ACID LIGANDS AND INHIBITORS
 NUMBER OF SEQUENCES: 89
 CORRESPONDENCE ADDRESS:
 ADDRESS: Swanson and Bratschan, L.L.C.
 STREET: 8400 East Prentice Avenue, Suite #200
 CITY: Denver
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
 COMPUTER: IBM compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WordPerfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/458,423A
 FILING DATE: 2-JUNE-1995
 CLASSIFICATION: 536

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/74,131
 FILING DATE: 10-JUNE-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/536,428
 FILING DATE: 11-JUNE-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/964,524
 FILING DATE: 21-OCTOBER-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 06/117,991
 FILING DATE: 8-SEPTEMBER-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/931,473
 FILING DATE: 17-AUGUST-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Diane H. McClellin
 REGISTRATION NUMBER: 960
 REFERENCE/DOCKET NUMBER: NEX 34.1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 753-3333
 TELEFAX: (303) 793-3433
 INFORMATION FOR SEQ ID NO: 78:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 71 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 US-08-458-423A-78

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 Best Local Similarity 65.54; Pred. No. 1.2e+03;
 Matches 36: Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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 Db 56 GAAGAGCTAAGTAAGTAGTATTATTAAGACATACCCCTCTGCGCCATGCTCTCTCC 2

RESULT 6
 US-08-458-424B-78/C
 Sequence 78: Application US/08/458424B
 Patent No. 5731424
 GENERAL INFORMATION:
 APPLICANT: PENELOPE J. TOOTHMAN
 APPLICANT: STEVEN RINGQUIST
 TITLE OF INVENTION: HIGH AFFINITY IGFA NUCLEIC
 ACID LIGANDS AND INHIBITORS
 NUMBER OF SEQUENCES: 89
 CORRESPONDENCE ADDRESS:
 ADDRESS: Swanson and Bratschan, L.L.C.
 STREET: 8400 East Prentice Avenue, Suite #200
 CITY: Denver
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
 COMPUTER: IBM compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WordPerfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/458,424B
 FILING DATE: 2-JUNE-1995
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/74,131
 FILING DATE: 10-JUNE-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/536,428

FILING DATE: 05-JUNE-1995
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/465,591
 FILING DATE: 05-JUNE-1995
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/479,725
 FILING DATE: 07-JUNE-1995
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/479,783
 FILING DATE: 07-JUNE-1995
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/618,693
 FILING DATE: 20-MARCH-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: BARRY J. SWANSON
 REGISTRATION NUMBER: 31,215
 REFERENCE/DOCKET NUMBER:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 793-3333
 TELEFAX: (303) 793-3433
 INFORMATION FOR SEQ ID NO: 78:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 71 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA

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Query Match      0.56; Score 24.6; DB 4; Length 71;
Best Local Similarity 65.53; Pred. No. 1.2e+03;
Matches 36; Conservative 19; Mismatches 19; Indels 0; Gaps 0;

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56 GAAGACGTAAGTAACTATTATAAACATACCCCCCTGGCGGATGCTGCC 2
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Search completed: May 29, 2002, 12:56:56
Job time: 9655 sec